

Fig. 1

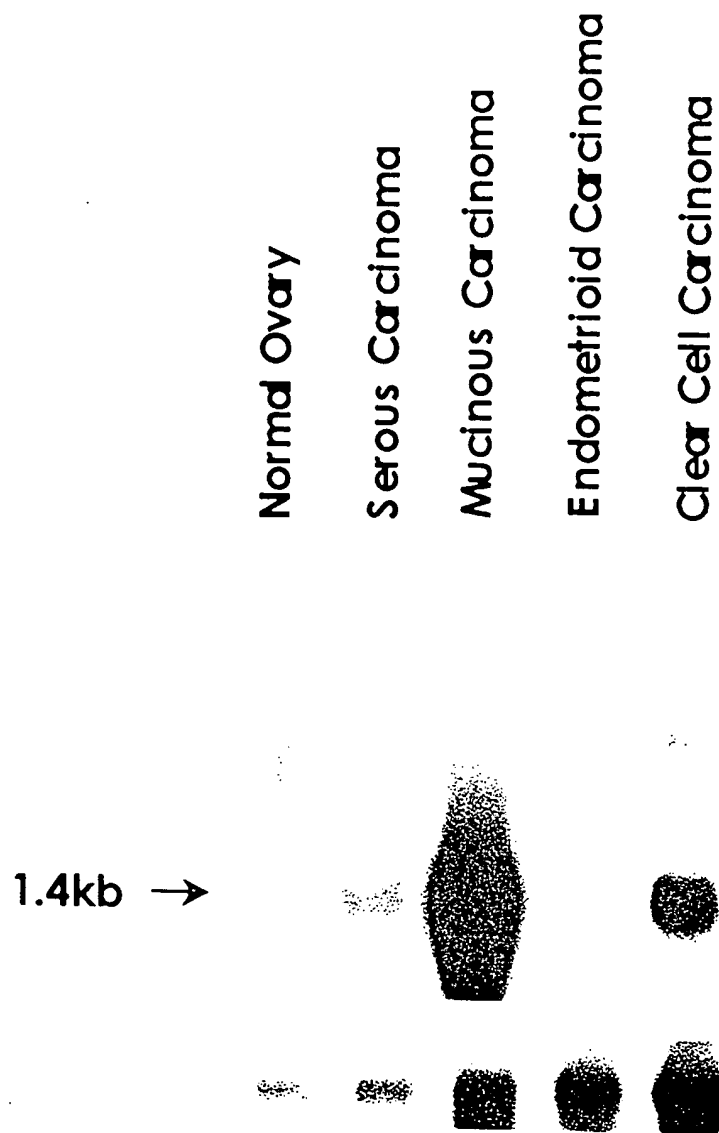


Fig. 2A

## FETAL

Brain

Lung

Liver

Kidney



Fig. 2B

## ADULT

Spleen  
Thymus  
Prostate  
Testes  
Ovary  
Small Intestine  
Colon  
P.B. Leukocyte\*

← TADG14



←  $\beta$ -tubulin

C

\* P.B. : Peripheral Blood

Fig. 2C

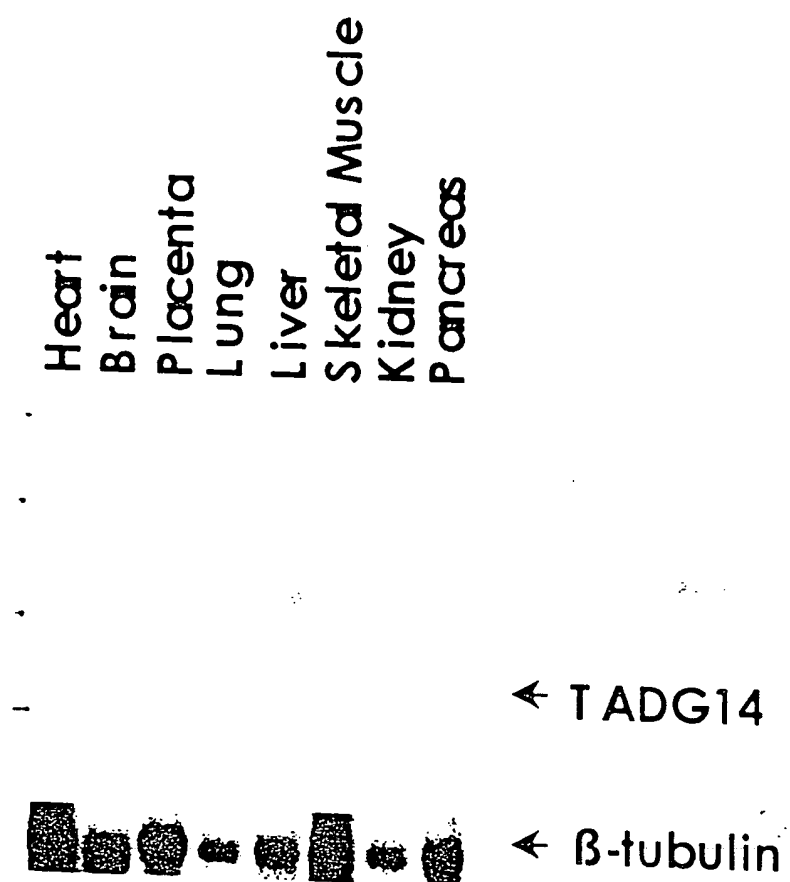


Fig. 2D

1 CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAACCTCAAATGGAAGAAATACCTTATGAATGTAAGAAATGTAGGGGGTCA 80  
81 TGGCTTGTAATTTACACAGTGTAAATGAAACCATCTAGAGGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAG 160  
161 CAAGCAAGAAAGGCTCCAGTGTCAAGGTAGTTTCAGCTCTTACAGGATATAAAACAGTCCATACCTTGAGAGAAAAAACTTA 240  
241 GATCTGAGTGTAGGAATGTGAAGCAAATCTTTCAAATCAGTAGACATTTCTTGACATATAAAACACAGATGAGGAAAGGG 320  
321 GTTCAAATTAGAAGTTACGTAATACCATCAGAAAGTTTCATGTTGGTAAATTTCTTACTAGAAATGTAGGAAATTCAG 400  
401 GTATAGCTTTGAATCCCAATTACACATTTGGTCAAGTGGGAAACTAAGGGCTCCAAACAGGCAAAATTCAGGGAGGATAGGT 480  
481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTTACCATGGGACGCCCCCGACCTCGTGGCGGCAAGACGTGGATGTTCCCTG 560  
M G R P R P R A A K T W M F L  
561 CTCTTGCTGGGGAGCCTGGCAGGACACTCCAGGGCACAGGAGGACAAGTGTCTGGGGGTTCATGAGTGCCCAACCCCA 640  
L L L G G A W A G H S R A Q E D K V L G G H E C Q P H  
641 TTCCGACGCTTGGCAGGCGGCTTGTTCAGGGCCAGCACTACTCTGTGGCGGTGTCTTGTAGGTGGCAACTGGGTCC 720  
S Q P W Q A A L F Q G Q Q L L C G G V L V G G N W V L  
721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCTGGGAGACCACAGCCCTACAGAAATAAAGATGGCCACAG T A A H C K K P K Y T V R L G D H S L Q N K D G P E  
801 CAAGAAATACCTGTGTTCACTCCACACCCCTGTACAAACAGCAGCGATGTGGAGGCCAACCATGATCTGAT Q E I P V V Q S I P H P C Y N S S D V E D H N H D L M  
881 GCTTCTTCAACTGCGTGACCGATCCCTGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTTGCACCCAGCCTG L L Q L R D Q A S L G S K V K P I S L A D H C T Q P G  
961 GCCAGAAGTGCACCGTCTCAGGCTGGGCACTGTCAACAGTCCCGAGAGAATTTTCCTGACACTCTCAACTGTGCAGAA Q K C T V S G W G T V T S P R E N F P D T L N C A E  
1041 GTAAAAATCTTTCCCCAGAGAAGTGTGAGGATGCTTACCCGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGAG V K I F P Q K K C E D A Y P G Q I T D G M V C A G S S  
1121 CAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGGCCCTCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGG K G A D T C Q G D S G G P L V C D G A L Q G I T S W G  
1201 GCTCAGACCCCTGTGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGTACCTGGACTGGATCAAGAAGATC S D P C G R S D K P G V Y T N I C R Y L D W I K K I  
1281 ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTATAAACTCACGGAATTC SEQ ID NO. 7  
I G S K G \* SEQ ID NO. 6

       = Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

       = Poly - adenylation signal

       = Conserved nt of catalytic triad

O = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Fig. 3A

hHk2	~~~~~MW	FLVLCIALSL	GCTGAAPPIQ	SRTVGGWECE	QHSQPWQAAL	42
hPSA	~~~~~MW	VPVFLTLVS	TWIGAAPLIL	SRTVGGWECE	KHSQPWQVLV	42
mNeur	MGRPPPCAIO	PWILLLLFMG	AWAGLTRAQG	SKILEGRECI	PHSQPWQAAL	50
hTADG14	MGRPRPRAAK	TWMFLLELGG	AWAGHSRAQE	DKVLGGHECQ	PHSQPWQAAL	50
hProm	~~~~~MKK	LMVLSLIAA	AWA...EEQ	NKLVHGGPCD	KTSHPYQAAL	39
hHk2	YHFSTFQCGG	ILVHRQWVLT	AAHCISDNMQ	LWLGRHNLFD	DENTAQFVHV	92
hPSA	ASRGRAVECG	VLVHPQWVLT	AAHCIRNKSV	ILLGRHSLFH	PEDTGQVFQV	92
mNeur	FQGERLICGG	VLVGDRWVLT	AAHCKKQKYS	VRLGDHSLQS	RDQPEQEIQV	100
hTADG14	FQGQQLLGG	VLVGGNWVLT	AAHCKKPKYT	VRLGDHSLQN	KDGPEQEIQV	100
hProm	YTSCHLLCGG	VLIHPLWVLT	AAHCKKPNLQ	VFLGKHNLQ	RESSQEQSSV	89
hHk2	SESFPHPGFN	MSLLENHTRQ	ADEDYSHDLM	LLRLTEPADT	ITDAVKVVEL	142
hPSA	SHSFPHPLYD	MSLLKNRFLR	PGDDSSHDEM	LLRLSEPAE.	LTDAVKVMDL	141
mNeur	AQSIQHPCYN	NS.....	NPEDHSHDIM	LLRLQNSAN.	LGDKVKPVQL	141
hTADG14	VQSIQHPCYN	SS.....	DVEDHSHDEM	LLRLQRDQAS.	LGSKVKPISL	141
hProm	VRAVIHBDY.	.....	DAASHDQDIM	LLRLARPAK.	LSELIQPLPL	127
hHk2	PTQEREVCGST	CLASGWCISIE	PENFSEPDLL	QCVDLKILPN	DECEKAHVQK	192
hPSA	PTQEPALCIT	CYASGWCISIE	PEEFLTPKKL	QCVDLHVISN	DVCAQVHPQK	191
mNeur	ANLCPKVQOK	CIISGWGTVT	SPOENFPNTL	NCAEVKITYSQ	NKGERAYPGK	191
hTADG14	ADHC'TQPQOK	CTVSGWGTVT	SPRENFPDIL	NCAEVKIFPQ	KKCEDAYPGQ	191
hProm	ERDCSANTTS	CHILGWGKTA	D..GDFPDIT	QCAIYIHLVSR	EECEHAYPGQ	175
hHk2	VTDFMLCVGH	LEGKDTCVG	DSGGPLMCDG	VLOGVTSWGY	VPCGTPNKPS	242
hPSA	VTKFMLCAGR	WTGKRSTCSG	DSGGPLVONG	VLOGITSWGS	EPCALPERPS	241
mNeur	ITEGMVCAGS	SN.GADTCQG	DSGGPLVCDG	MLOGITSWGS	DPCGKPEKPG	240
hTADG14	ITDGMVCAGS	SK.GADTCQG	DSGGPLVCDG	ALOGITSWGS	DPCGRSDKPG	240
hProm	ITQNMLCAGD	EKYGKDSQCG	DSGGPLVCGD	HLRGLVSWGN	IPCGSKEKPG	225
hHk2	VAVRVLSYVK	WIETIAENS	SEQ ID NO: 9			262
hPSA	LYTKVAVHVRK	WIKDTIVANP	SEQ ID NO: 10			261
mNeur	VYTKICRYTT	WIKKTMNDRD	SEQ ID NO: 8			260
hTADG14	VYTNICRYLD	WIKKIIGSKG	SEQ ID NO: 7			260
hProm	VYTNVCRYTN	WIKKTIQAK-	SEQ ID NO: 11			244

Fig. 3B

[illegible]

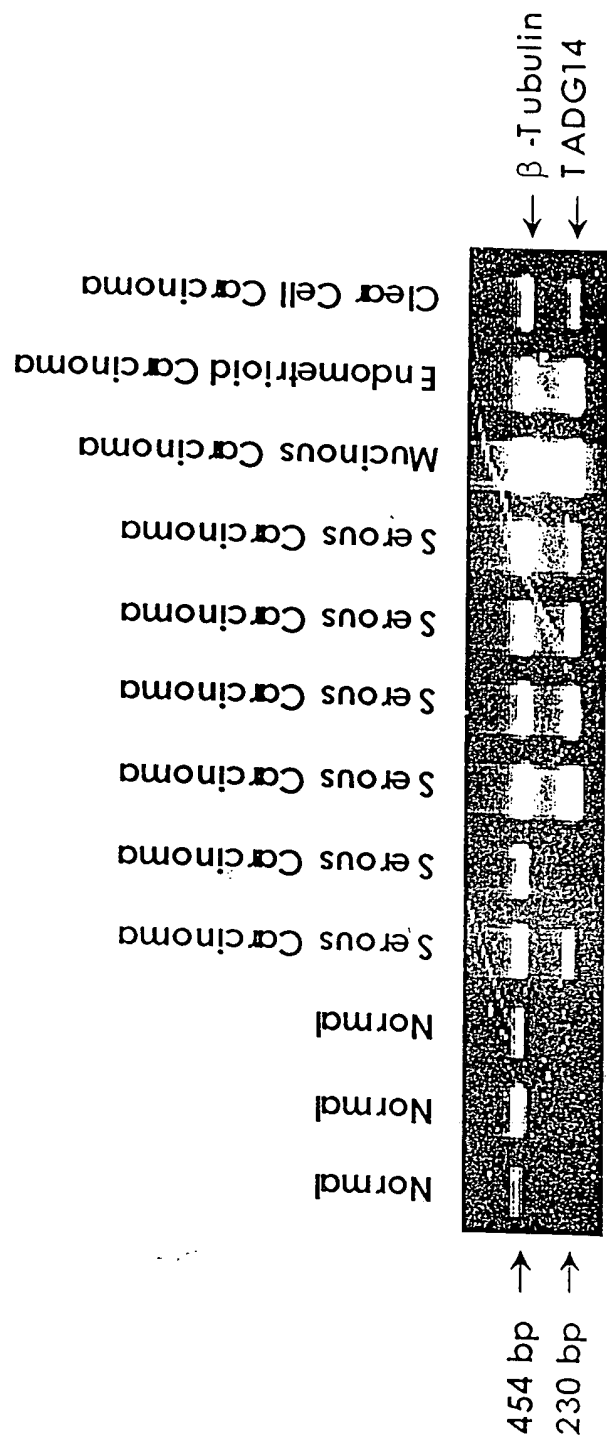


Fig. 5A

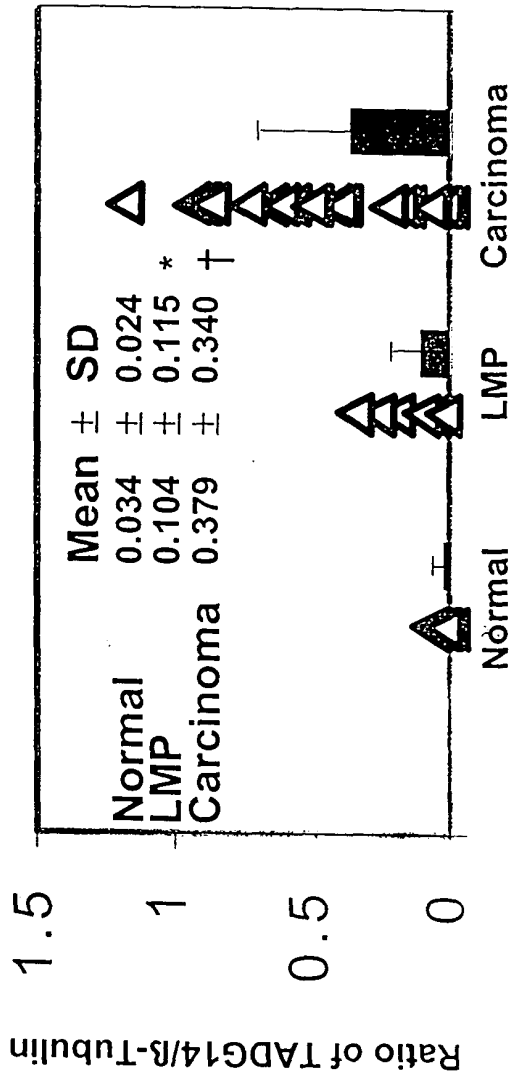


Fig. 5B

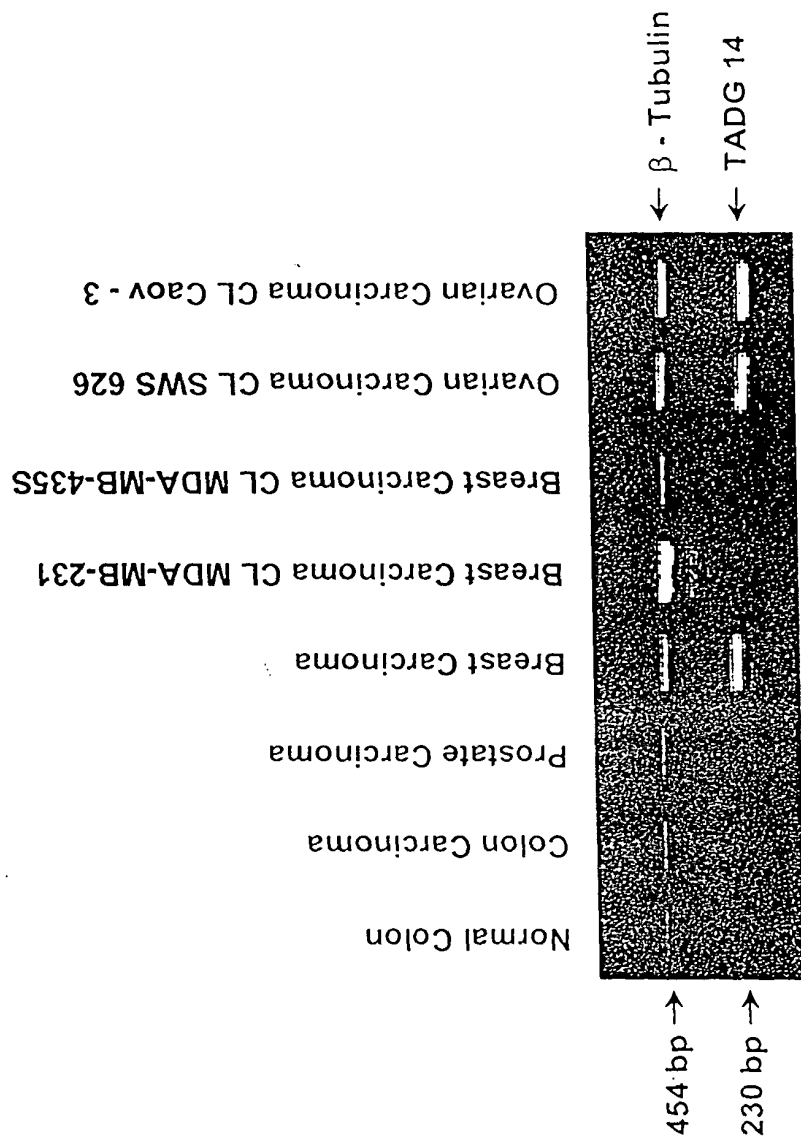


Fig. 6

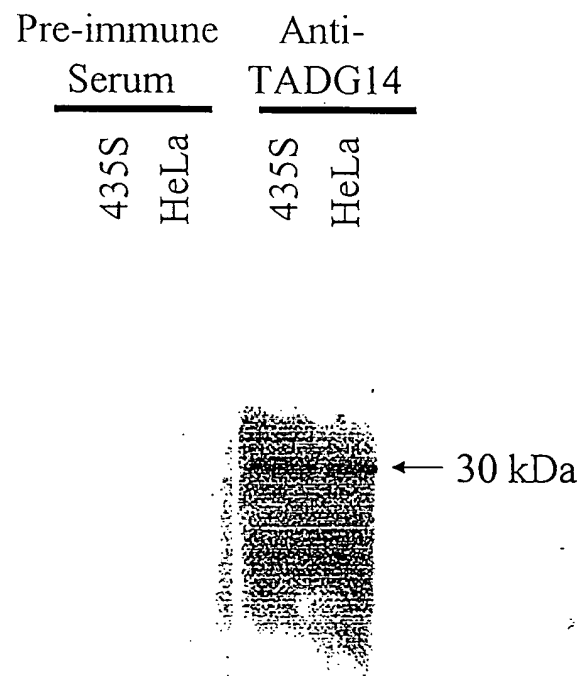


Fig. 7

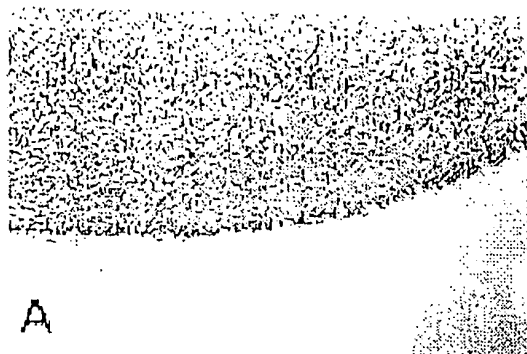


Fig. 8A

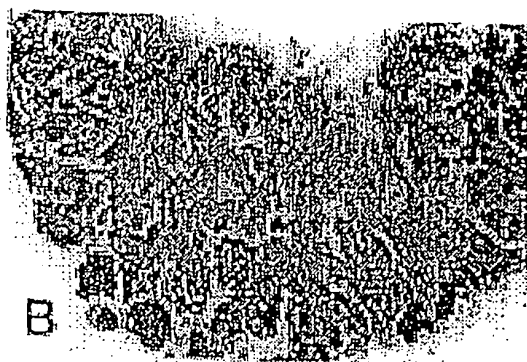


Fig. 8B



Fig. 8C

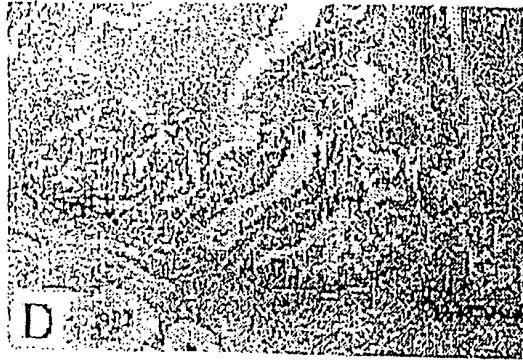


Fig. 8D



Fig. 8E

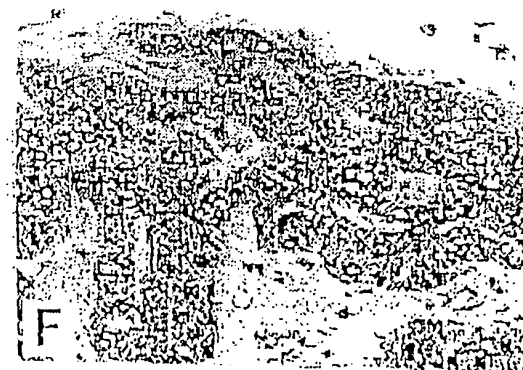
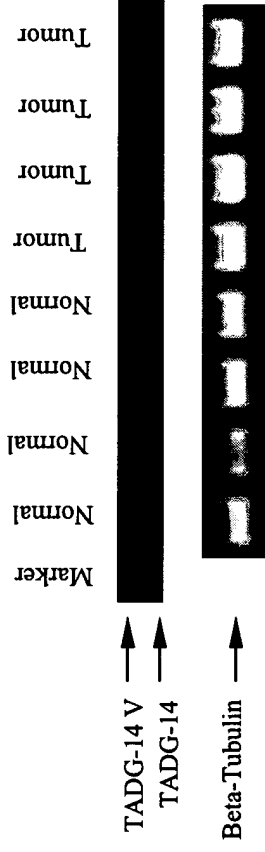
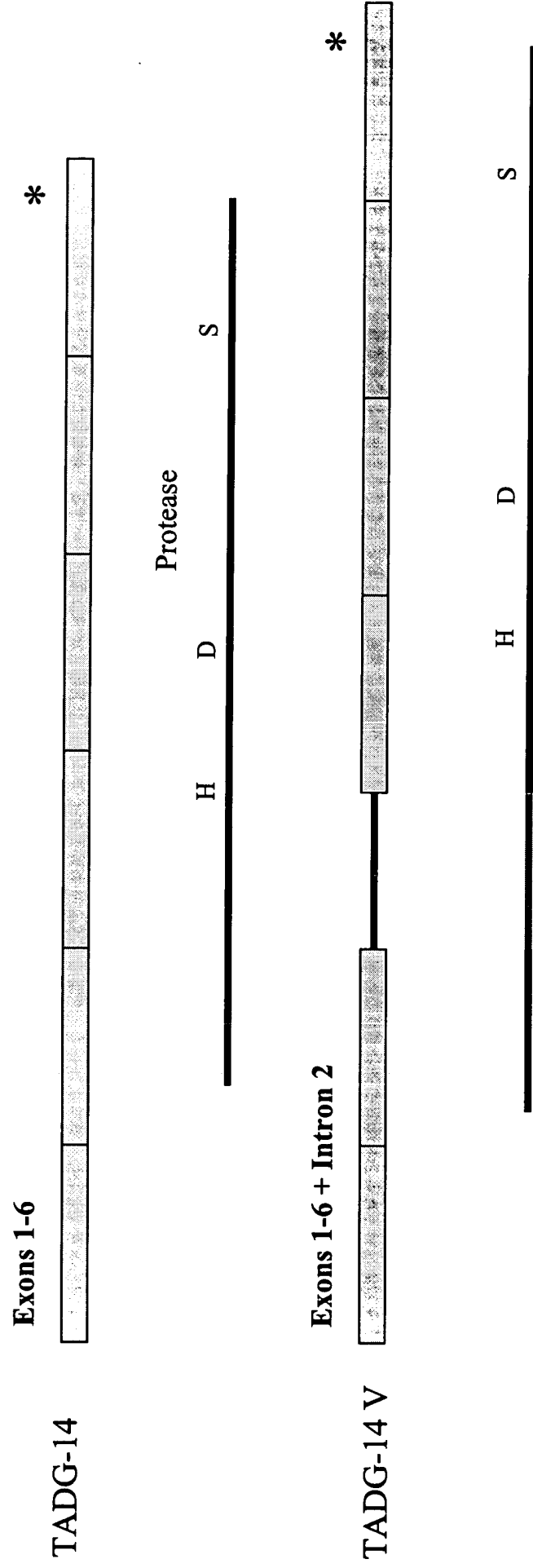


Fig. 8F



**Fig. 9**



**Fig. 10**

Tadg 14	MGRPRPRAAK	TWMFLLLLLG	AWA.....	.....
Tadg 14 V	MGRPRPRAAK	TWMFLLLLLG	AWAACGSLDL	LTKLYAENLP CVHLNPQWPS
Tadg 14	.....	.....GH	SRAQEDKVLG	GHECQPHSQP WQAALFQGQQ
Tadg 14 V	QPSHCPRGWR	SNPLPPAAGH	SRAQEDKVLG	GHECQPHSQP WQAALFQGQQ
Tadg 14	LLCGGVLVGG	NWVLTAAHCK	KPKYTVRLGD	HSLQNKDGPE QEIPVVQSIP
Tadg 14 V	LLCGGVLVGG	NWVLTAAHCK	KPKYTVRLGD	HSLQNKDGPE QEIPVVQSIP
Tadg 14	HPCYNSSDVE	DHNHDLMLLQ	LRDQASLGSK	VKPISLADHC TQPGQKCTVS
Tadg 14 V	HPCYNSSDVE	DHNHDLMLLQ	LRDQASLGSK	VKPISLADHC TQPGQKCTVS
Tadg 14	GWGTVTSPRE	NFPDTLNCAE	VKIFPQKKCE	DAYPGQITDG MVCAGSSKGA
Tadg 14 V	GWGTVTSPRE	NFPDTLNCAE	VKIFPQKKCE	DAYPGQITDG MVCAGSSKGA
Tadg 14	DTCQGDSSGP	LVCDGALQGI	TSWGSDPCGR	SDKPGVYTNI CRYLDWIKKI
Tadg 14 V	DTCQGDSSGP	LVCDGALQGI	TSWGSDPCGR	SDKPGVYTNI CRYLDWIKKI
Tadg 14	IGSKG (SEQ ID NO. 7)			
Tadg 14 V	IGSKG (SEQ ID NO. 75)			

Fig. 11